

Db 241 EEGEEQSDNPYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNYRLVLEANPNA 300
QY 241 EEGEEQSDNPYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNYRLVLEANPNA 300
Db 301 FVLPHLDADALLVYGGGALKMTHDNRRESYNLECGVIRIPAGTFFYLINRDNNEEL 360
QY 301 FVLPHLDADALLVYGGGALKMTHDNRRESYNLECGVIRIPAGTFFYLINRDNNEEL 360
Db 361 HTAKFLQITSTPGQYKEFFPAGGONPEPYLSTFESKELLEALNTQETKLRGVFGQOREGV 420
QY 361 HTAKFLQITSTPGQYKEFFPAGGONPEPYLSTFESKELLEALNTQETKLRGVFGQOREGV 420
Db 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGQAYEVKPEDYR 480
QY 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGQAYEVKPEDYR 480
Db 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVYVAGSADVEMACPHLSGRHGRGGGR 540
QY 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVYVAGSADVEMACPHLSGRHGRGGGR 540
Db 541 HEEEDVHYEQYKARLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600
QY 541 HEEEDVHYEQYKARLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600
Db 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDOSIFFPGPROHQOQSPRSTKQOQPLYSI 660
QY 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDOSIFFPGPROHQOQSPRSTKQOQPLYSI 660
Db 661 LDFVGF 666
QY 661 LDFVGF 666

RESULT 2
ID W62829 standard; Protein: 666 AA.
AC W62829; 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 39-41; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 96.4%; Score 4746; DB 1; Length 666;
Best Local Similarity 96.1%; Pred. No. 0.00e+00;
Matches 640; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

Db 1 MAINSNSCLSLFLSLSTVSLAESEPDROVEECKRCOMOLETSGNRCVSCOD 60
QY 1 MAINSNSCLSLFLSLSTVSLAESEPDROVEECKRCOMOLETSGNRCVSCOD 60
Db 61 KREEDIDMSKYNDODDPTDCOCCORRCROESGPROQOYCORCKECEESEYENQR 120
QY 61 KREEDIDMSKYNDODDPTDCOCCORRCROESGPROQOYCORCKECEESEYENQR 120

Db 121 DPOQYEOCOERCOHETEPHNMOTCOORCERRYEKEKROOKRYEEOQREDEKEERYEM 180
QY 121 DPOQYEOCOERCOHETEPHNMOTCOORCERRYEKEKROOKRYEEOQREDEKEERYEM 180
Db 181 KEEDKRRPOOREYEDCRRRCEDQOEPROQYOCORRCROQROHGRGGLINPQGGSSRY 240
QY 181 KEEDKRRPOOREYEDCRRRCEDQOEPROQYOCORRCROQROHGRGGLINPQGGSSRY 240
Db 241 EEGEEQSDNPYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNYRLVLEANPNA 300
QY 241 EEGEEQSDNPYFDERLSSTRFTEEGHISYLENFYGRSKLLRALKNYRLVLEANPNA 300
Db 301 FVLPHLDADALLVYGGGALKMTHDNRRESYNLECGVIRIPAGTFFYLINRDNNEEL 360
QY 301 FVLPHLDADALLVYGGGALKMTHDNRRESYNLECGVIRIPAGTFFYLINRDNNEEL 360
Db 361 HTAKFLQITSTPGQYKEFFPAGGONPEPYLSTFESKELLEALNTQETKLRGVFGQOREGV 420
QY 361 HTAKFLQITSTPGQYKEFFPAGGONPEPYLSTFESKELLEALNTQETKLRGVFGQOREGV 420
Db 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGQAYEVKPEDYR 480
QY 421 IIRASQEOIRELTRDSDSRHWHIRRGESSRGPNLFNKRPPLYSNKYGQAYEVKPEDYR 480
Db 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVYVAGSADVEMACPHLSGRHGRGGGR 540
QY 481 OLQDMDSLVSFIANTVQSGMMGPFFNTRSTKVVVYVAGSADVEMACPHLSGRHGRGGGR 540
Db 541 HEEEDVHYEQYKARLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600
QY 541 HEEEDVHYEQYKARLSKREAIYVLAGHPVYVSSGNENLLFAFGINAQNNHNEFLAGR 600
Db 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDOSIFFPGPROHQOQSPRSTKQOQPLYSI 660
QY 601 ERNVLOQIEPQAMELAFAPRKREVEESFNSDOSIFFPGPROHQOQSPRSTKQOQPLYSI 660
Db 661 LDFVGF 666
QY 661 LDFVGF 666

RESULT 3
ID W62830 standard; Protein: 625 AA.
AC W62830; 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 43-45; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 625 AA;

Query Match 91.1%; Score 4487; DB 1; Length 625;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 604; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

D	b	1	OCMOLETSQGNMRCVSCQCDKRFEDIDMSKTDNDNEDPOTECQCCQRCRCROEESP	60
O	y	42	OCMOLETSQGNMRCVSCQCDKRFEDIDMSKTDNDNEDPOTECQCCQRCRCROEESP	101
D	b	61	CQRCKEICEEHEEENNRQDPQOQYEQCCQRCORRETEPRHMQICQOORCERYE	120
O	y	102	CQRCKEICEEHEEENNRQDPQOQYEQCCQRCORRETEPRHMQICQOORCERYE	161
D	b	121	QKRYEQQREDEBEKEYEERKMGDNKRDPOQREYEDCRRHCEQOEPRLOQCQRR	180
O	y	162	QKRYEQQREDEBEKEYEERKMGDNKRDPOQREYEDCRRHCEQOEPRLOQCQRR	221
D	b	181	OHGRGCDLMNROGSSGSGYEGEKQSNRPYEDERSLSTFEFRREBHISYLEN	240
O	y	222	OHGRGCDLMNROGSSGSGYEGEKQSNRPYEDERSLSTFEFRREBHISYLEN	281
D	b	241	LLRALKNRYLVLEAPNPAFVLPNHLADAILVIGGRGALKMIRHNRRESYNLE	300
O	y	282	LLRALKNRYLVLEAPNPAFVLPNHLADAILVIGGRGALKMIRHNRRESYNLE	341
D	b	301	RIPAGTFTYLLNRDNNEERLHIAKTLQITSTPGQYKEFFPAGQNPDEYLS	360
O	y	342	RIPAGTFTYLLNRDNNEERLHIAKTLQITSTPGQYKEFFPAGQNPDEYLS	401
D	b	361	LNTOGERLRGVLAGOORESVIIIRASOEQIRRELTTRDSSRRMHIIRGESS	420
O	y	402	LNTOGERLRGVLAGOORESVIIIRASOEQIRRELTTRDSSRRMHIIRGESS	461
D	b	421	PLYSNKYQGAAYEVPEDYRQLODMQDVSVFIANIQSGMMGPFENRTSKYV	480
O	y	462	PLYSNKYQGAAYEVPEDYRQLODMQDVSVFIANIQSGMMGPFENRTSKYV	521
D	b	481	EMACPHLSGRHGGGGGGRHHEEVEHYEYVRAFLSKREALVVLAGHPV	540
O	y	522	EMACPHLSGRHGGGGGGRHHEEVEHYEYVRAFLSKREALVVLAGHPV	581
D	b	541	LEAFGINQNNHNEHFLAGRENNVLOQIEPOMELTAFASREVEELN	600
O	y	582	LEAFGINQNNHNEHFLAGRENNVLOQIEPOMELTAFAPKREVEESN	641
D	b	601	QHQQQSPRSTKQOQPLVSIIDFVGF	625
O	y	642	QHQQQSPRSTKQOQPLVSIIDFVGF	666
RESULT 4				
ID	R20181 standard; Protein; 566 AA.			
AC	R20181;			
DT	16-APR-1992 (first entry)			
DE	Sequence encoded by 67 kd T. cacao protein cDNA.			
KW	Cocoa: flavour; vicillin; seed storage protein.			
OS	Theobroma cacao.			
PN	W09119801-A.			
PD	26-DEC-1991.			
PF	07-JUN-1991: G00914.			
PR	11-JUN-1990: GB-013016.			
PA	(MRSC.) MARS UK LTD.			
PI	Spencer ME, Hodge R, Deakin EA, Ashton S;			
DR	WPI: 92-024418/03.			
NR	P-PSDB: Q20377.			
PT	Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial expression vectors			
PS	Claim 4; Fig 2; 59pp; English.			
CC	The inventors claim a 67 kD and 31 kD T. cacao protein, and fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacao protein cDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBR peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close			
CC	homologies between the 67 kD polypeptide and the vicillins, which are seed storage proteins.			

Sequence 566 AA; Score 1246; DB 1; Length 590;

Query Match 27.0%; Score 1330; DB 1; Length 566;
Best Local Similarity 39.7%; Pred. No. 4,66e-106;
Matches 215; Conservative 146; Mismatches 153; Indels 27; Gaps 21.

Dd ERDPQOYECORCESE-AATEEREE-QCE--ORCERE-YKEGROOE--E-LONGOY 86
|::||:|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy ETEPHM-OHQQRERRERYEKKKKQARYEQOREDEBEKEEEKMKEDNKRDOOREYE 195
Dd OCGGCOEOGOOGORBOOCCKWCKEYKEODRGESHVHNHK-KNRSEEEOGRNNPY 145
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy DCRRC-EQE-PHQHCQLRCEQORQHRRGDMMNPORGSGRREBEGESDMPY 253
Dd FPKRSFOTREFDEGNFKILQREAFNSPPLKINDYRLAMEANPTFILPHHCAEI 205
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy FEDR-SLSTRTERTEGHSTVLNFYGRSKLLRALKNRYLVLEAPNAFVLPHTLDADI 312
Dd YFYNGKGTITFYHENKESINVRGVSVSPASTIYYVSQDNQELTAVLAIPVNSP 265
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy LLVIGRQALMIHHNDNESYNLCGGVIRLPACTFEYLINRDNNRHIAKFLQITSTP 372
Dd GKYLEFPAGNNKPESYASVYLEVFNTOREKLEILEBOROKROGOOGMRKA 325
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy GOYKEFPAGONPEPIYSTSKILLEALTQTEKLRGVFGGOGBEVITRASQETREL 432
Dd KPDTRAIQSQTSPRRGERLAINLSOSPVYSNONGRFFECAPDESOFQMADVAVS 385
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy TRDD--SSRMWHIRRGESSRGYNLFENRPLTSNKYGAEVKRPDYROLDMDSVF 450
Dd AFKLNGAIEVPYHNSKATVEVTDCGYAQMACPLSRQSOSSQSGDRDRREEESE 445
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy IANTOGSMGPFTNSTRTSKVVVAASEADVENACPLSLGR-HGRRGC-GKR-HEEE-- 544
Dd EEETGEPOVAKPSIDPGDVFAFPAHGVTFEPASDOGLNAVAGSLANNONRIFLACK-X 504
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy EDV--HYEQVARLSKREDAIVLGHHPVYVSSGENELLFAGGINQNHNHENLAGRRR 602
Dd NLVRQMSAEKLEFGVPSKLVADIFNNPPDES-VFNSFSO-QOR-RDERGNPLASILD 561
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Qy NVLQIQEAQAEIAFAPRKVESESFNSODSIFFPPRQHQQOSPSTKQQQPLVSIID 662

Dd 562 F 562.
|
Qy 663 F 663

RESULT 5
ID W62832 standard; Protein; 590 AA.
AC W62832;
DT 27-OCT-1998 (first entry)
DE Gossypium hirsutum antimicrobial protein.
KM antimicrobial protein; instestation; control.
KS Gossypium hirsutum.
PN WC9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
RA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulier CK, Green JL, Manners JM, Marcus JP;
DR WPJ; 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PS useful for controlling microbial infestations of plants or mammals
CC Claim 1, Page 49-51, 96pp; English.
The sequence is that of an antimicrobial protein which can
be used to control microbial infestations in plants and mammalian
animals.
SQ Sequence 590 AA;

Query Match 25.3%; Score 1246; DB 1; Length 590;
Best Local Similarity 39.5%; Pred. No. 2.04e-98;
Matches 223; Conservative 150; Mismatches 144; Indels 47; Gaps 29;

Db 36 DPKRVEDCRRCRCEWDTGKCEKQCEESKSGYGEKQDQQRHREDPDRYRECEQCECR 95
121 DPQOQYECOKHCKORRETERPHMOTCOQRCERY-EKEK--R-K-Q--QRYEE-QQ--R 170
Db 96 QOEERQOPQOQOKLKEFEDEQOOSOROFQECQCHQOORPKKQOQRECEKXQEN 155
171 EDEK---YEER-MKEDNKRDOQREYEDCRRCQEQERPOQ--HOCOLRCRQOQOH 223
Db 156 PMRGER-EEEAEEET-EEGEQESHNPFFHRRSFOSRFEHGNFVLRQFASRHPIL 213
224 GRGDDMMNPRGSGRGREBEDEBQSDNPRYFDERSLSTRTEEGHISVLENFYGRSKL 263
Db 214 RGINEFRLSLBANPTFVLPHCDAKIYLVINGRCTLFLHENEKESNIVPGVYKV 273
284 RALKNYRLVLEENPNFVPTHLADAILLVIGRGALMHIHNDRESYNLECGDVIRI 343
Db 274 PASTVLANODNKEKILIVLHPRVNPQOFEEFPAGSORPOSYRARSRILEPFAFN 333
344 PAGTFYLRNDNERRHIAKFLQTLSTPGQYKEFPAGQONPEPYLSTFSKELLEALN 403
Db 334 TRSELDLDFGGRSRRRQOGGMRKASQEOIRALSQEAITSRE--KSQE--REAFN 387
404 TQREKLNGVFG--Q--QRE-G-VIIR-ASQOIRRELRDSESHMHIRRGESSRGPYN 456
Db 388 LLSOTPRYSNONGRFFECPCPEERQDLINVTYSALQNGSIFVPHYNSKATFVILYTE 447
457 LFNKRPYSNKGQAYEVKPEDEYROLQMDLSVFIVANTQSGMGPFFNRSTKVVYVAS 516
Db 448 GNCYAEVNSHPLROSSYEEDEEEDDEEEOEERSSGQYRKRSRSLSGDIFVYVAFN 507
517 GEADEVACPHL--SG--RHGRGGGKRHEED--V-HYEOVRALSRREAVLAGH 568
Db 508 PTFVVASQONLMTGGLXNQNINPDHONRIFVAKINHV-RQMDSQAKELAFGVSSRL 566
569 PVFVSSGNNLLFAGGINAON--N--H-EN-FLAGERRVLIQIPEQAMELAFAPRKE 623
Db 567 VDFEFSNPQESTFVS-RQORAS 569
624 VEEFSNQDOSIFFPGRHOQOS 647

RESULT

ID W62831 standard; Protein: 525 AA.

AC W62831;

DT 27-OCT-1998 (first entry)

DE Theobroma cacao antimicrobial protein.

KW antimicrobial protein; infestation; control.

OS Theobroma cacao.

PN WO9827805-A1.

PD 02-JUL-1998.

PF 22-DEC-1997; AU0874.

PR 20-DEC-1996; AU-004275.

PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

PI Bower NJ, Goulter KC, Green JL, Manners JM, Marcus JP;

DR WPI: 98-377279/32.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -

PS Claim 1; Page 47-49; 96pp; English.

CC The sequence is that of an antimicrobial protein which can

CC be used to control microbial infestations in plants and mammalian

CC animals.

SQ Sequence 525 AA;

Query Match 23.9%; Score 1178; DB 1; Length 525;
Best Local Similarity 40.0%; Pred. No. 3,056-92;

Matches 191; Conservative 125; Mismatches 139; Indels 23; Gaps 17;

Db 35 ERPPROQYEQRCRCESE-ATEERDE-QCE--QRCERE-YKEQOQOE--E-LQROQ 86
137 ETEPRHML-QTCOORCERREYKEREKQKQRYEEOQREDEYEEERMKEDNKRPOQOHE 195
Db 87 QCGRGCEQO 145

QY 196 DCRRC-EDQE-PROHOCOLRCRQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 253
Db 146 FPKRSFOTRFEDEENFALOFNAENSPRLGINDYRLAMEANENPILPHHCDAEAI 205
254 FDR-SLSTRFRFEHISVLENFYGRSKLRLKKNRYLVLEANPNFVPTHLADAI 312
Db 206 YETNKGITTEFTYHNKESYNQKCTVSVRAGSVYVVSQDNOCKLIVLALPVNSP 265
313 LVIIGRGALMHIHNDRESYNLECGDVIRIPAGTFYLRNDNERRHIAKFLQTLSTP 372
Db 266 GKYLEFPAGNNPESYGAESYLETEVNTQREKLEELIEBQORQOQOQOQOQOQOQO 325
373 GQYKEFPAGQONPEPYLSTFSKELLEALNTQTEKRVFGQQRGVYIRASQOIREL 432
QY 433 TRDD--SESHMHIRRGESSRGPYNLFNKRPYSNKGQAYEVKREDEYROLQMDLSVF 490
Db 386 AFLNGALFVPHYNSKATFVFTDGYGAQACHLSROSQOSQOQOQOQOQOQOQOQO 445
491 IANTQSGMGPFFNRSTKVVYVASGEADVACPHLSGR-HGGRG--GR-HEE-- 544
QY 446 EETFGEOQKAPLSPGDYFVAPAGAVTFPASKDQPLAAVFGLAONNORIFLAGR 503
545 EDV--HYEOVRALSRREAVLAGHVVSVSGENLLFAGGINAONNHENFLAGR 600

RESULT

ID W62835 standard; Protein: 593 AA.

AC W62835;

DT 27-OCT-1998 (first entry)

DE Zea mays antimicrobial protein.

KW antimicrobial protein; infestation; control.

OS Zea mays.

PN WO9827805-A1.

PD 02-JUL-1998.

PF 22-DEC-1997; AU0874.

PR 20-DEC-1996; AU-004275.

PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

PI Bower NJ, Goulter KC, Green JL, Manners JM, Marcus JP;

DR WPI: 98-377279/32.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -

PS Claim 1; Page 58-60; 96pp; English.

CC The sequence is that of an antimicrobial protein which can

CC be used to control microbial infestations in plants and mammalian

CC animals.

SQ Sequence 593 AA;

Query Match 22.3%; Score 1099; DB 1; Length 593;
Best Local Similarity 40.4%; Pred. No. 4,416-85;

Matches 202; Conservative 113; Mismatches 156; Indels 29; Gaps 22;

Db 25 EDNNHHHGHGKSGOCVRCEDR-PWNOBRPLCEQREBERKQOERSHHEADRSGES 83
182 EEDNKKDPOQREYEDRRKCEQOERQOH-QCOLRCRQOQO--HCRGDDMMNPRQG-GS 237
Db 84 SEDEREQEKQKDRRPPYFDRSFRVRSQSLRVLRPDEVSRLLRGIRDYAVAV 143
238 GRE-EGEE-QSDN-PYFDERSLSTRTEEGHISVLENFYGRSKLRLKKNRYLV 294
Db 144 EANPSFVVPSTDAHCTVADGEGVTTIENGERRSTIQGHVFAVAPAGAVTYLANT 203
295 EANPNFVPTHLADAILLVIGRGALMHIHNDRESYNLECGDVIRIPAGTFYLRN 354
Db 204 DGRKTLVIRKIHTISVPEQFEFFPGGRNPESFSSKSIQRAYTSSDRLERLFG 263
355 DNNRHHIAKFLQTLSTPGQYKEFPAGQONPEPYLSTFSKELLEALNTQTEKLVG 414
Db 264 RHQDGIIVRATQETRELIRASGEGHPMLRPFGE--RGPSLLDQPSIANQ 322
415 QO--RE-GVIRASQOIRRELRDSES--R--HMHIRGESSRGPYNLFNKRPYSNKG 469

OY 367 Q-TISTPGQYKEFFPAGGONPEPYLSTFSKELLEALNTOTKEKRGVFGQOREGVIIRAS 425
DB 287 REOVBALAPTKKSSW-WPF--GGEES-KPOFNIFSKRPTISNGYRLTEVGPDDDEKSWLQ 342
OY 426 QOQIELTRDSESRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEKPEDY-RQ-LQ 483
DB 343 RLNLMLFTNTITORSNSTIHYNSHATKIALVIDRGHLQISCPHMSR--SSHS--K-HDK 398
OY 484 DMDLSVFIANVTOGSMGPFENRSTKVVVAVASGEADVEMACPHLSGRHGGGGRHDE 543
DB 399 SSPS-YHRISDLPKGMVFPVPGHFVTIASNKENLIMICEFVARDKK-KFTFAGKD- 455
OY 544 EEDVHYEQVRAKLSKREAVIVLAGHPVYVSSGNENLLFAFGINAKONHENT-LAGKER 602
DB 456 NIVSSLDNVAKELAFNYPSEMNGVF 481
OY 603 NVLQGLEPQAMELAFAPRKEVEESF 628
RESULT 10
ID W90340 standard; protein: 444 AA.
AC W90340;
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP1 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KM seed; carbohydrate content; soybean.
OS Glycine max.
PN W09853086-A1.
PD 26-NOV-1998.
PF 21-MAY-1998: U10465.
PR 22-MAY-1997: US-047568.
PI (UNIT) UNIV WASHINGTON STATE RES FOUND.
PA Chao WS, Gimes HD;
DR WPI, 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
transgenic plants which can have enhanced or decreased sucrose
uptake activity in developing seeds
PS Claim 7; Page 36-37; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
from glycine max. This protein is used in a method resulting in the
production of a modified plant sucrose binding protein (SBP) which has a
modified amino acid sequence compared to a corresponding wild-type SBP,
and where expression of the modified SBP in a yeast assay system confers
enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
which have modified sucrose uptake activity, particularly in developing
seeds. Enhanced sucrose uptake activity in developing seeds may be
desirable where it is an advantage to increase the carbohydrate content,
of the seed (e.g. where the seed is the primary plant material harvested,
such as soybean). In contrast, decreased sucrose uptake activity in
seeds might be desirable where the vegetative material of the plant is
harvested. The SBP regulatory regions confer specific or enhanced
expression in developing seeds and so may be used to express any
transgene in developing seeds.
CC Sequence 444 AA.

Query Match 19.6%; Score 964; DB 1; Length 444;
Best Local Similarity 38.8%; Pred. No. 6, 98e-73;
Matches 158; Conservative 109; Mismatches 123; Indels 17; Gaps 15;

DB 49 QOQYTEGDKRYCLOCDRIYHMKOERKQIO-EETRF-KKEEESREDEEOEOHEOD 106
OY 190 QOREY-EDCRRCEDOEPRQOQOQOLRCREOOROGRGDMNPNRGSGRAGEEES 248
DB 107 ENPYFEEDKDEETVETEGGRIRYLAKFKTEKSKLLOGIENRLAILTEARATVSPRNF 166
OY 249 DNPYFDE-RSSTSTRKEEGHISVENYGRSKLRALKNRLLVLEENPAFVLPPL 307
DB 167 DSEVVFENKRAVLGIVSESEKITLEPQGMHINIPAGTPYIYNRDENDLFLAMLHI 226
OY 308 DMDALILVIGSGALKMHIHNDRESYNLECGDVIIRPATFTYLLINRDNNEHLIAKF-L 366
DB 227 PYVSTPGKEFEFFAPGGRDPSVLSAHSWNLQALALQTPKGLLENVDQONEGSI 286

OY 367 Q-TISTPGQYKEFFPAGGONPEPYLSTFSKELLEALNTOTKEKRGVFGQOREGVIIRAS 425
DB 287 REOVBALAPTKKSSW-WPF--GGEES-KPOFNIFSKRPTISNGYRLTEVGPDDDEKSWLQ 342
OY 426 QOQIELTRDSESRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEKPEDY-RQ-LQ 483
DB 343 RLNLMLFTNTITORSNSTIHYNSHATKIALVIDRGHLQISCPHMSR--SSHS--K-HDK 398
OY 484 DMDLSVFIANVTOGSMGPFENRSTKVVVAVASGEADVEMACPHLSGRHGGGGRHDE 543
DB 399 SSPS-YHRISDLPKGMVFPVPGHFVTIASNKENLIMICEFVAR 444
OY 544 EEDVHYEQVRAKLSKREAVIVLAGHPVYVSSGNENLLFAFGINAO 590

RESULT 11
ID W62838 standard; protein: 605 AA.
AC W62838;
DT 27-OCT-1998 (first entry)
DE Glycine max antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Glycine max.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997: A00874.
PR 20-DEC-1996: AU-004275.
PI (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PA Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI, 98-372729/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 63-65; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
be used to control microbial infestations in plants and mammalian
CC animals.
CC Sequence 605 AA;

Query Match 18.9%; Score 930; DB 1; Length 605;
Best Local Similarity 32.7%; Pred. No. 8, 08e-70;
Matches 193; Conservative 160; Mismatches 197; Indels 41; Gaps 32;

DB 38 CLOCSNRSRDYRNA-CHARCNLIKVECECEGELTPRP-PRQ-HPEREPOQGEKE 94
OY 85 QCRKROQESPRQOYQQRCKELCEEEENRQROPOQOYEQOQKQRETEPRMQ 144
DB 95 EDEDE-OPR-PIPFPRPOP-OOEEHEOREE-OEWPRKEE-KRGKSEED-DEDEEO 148
OY 145 TCQQCERRYEKERKKQQRKEDEOREDEKYEERKEDNKRPOQREYEDCRRCQ 204
DB 149 DERQPPFRPHQKEERNEEDEDE-EOQRESEES-EDSELRRKKNKPNFLGSRNPE 206
OY 205 EPRQHQOQLCREQOQRHGRGDMNPNRGSGRYEGE-EEQSD-NPYFDEMSLSTR 262
DB 207 FKNQYGRIVLORENORSPOLONLDRYILEFNSKPTLLPNHADYLLVINGAIL 266
OY 263 FTEGHTSVLENFGRSKLRALKNRLLVLEENPAFVLPPTHIDDAIILVIGRGAL 322
DB 267 SLVNNDDSDSYRLQSGDLRVPSGTYVVPNDNNEHRLTLIAIPVKKPGRFSFELS 325
OY 323 KNIHNDNESTNLECGDVIIRPATFTYLLINRDNNEHLIAKFQIOTISTPGQYKEFPAG 382
DB 327 TEAOQYQGSRNILEASYDTKFEELIKVLFSEEGQOQOQOESVYIEISKEOIRA 386
OY 383 GONPEPYLSTFSKELLEALNTQ--TE--K-L-R--GVF-GQOR--EGVIRASQOQIRE 431
DB 387 LSKRAKSSRK-TI--SEED-K-PENLRSDPIYSNKGKFEFTPEKNPOLDLIFLS 441
OY 432 LT-RDSDSESRHWHIRRGESSRGYPNLFNKRPLXSNKYGAUYEAVKPEDYOLQMDLSVF 490
DB 442 IVDNNEGALLLPHFNSKALVILVINEGPAITELV-G-LKEGO--QE--QOQOEPLEVR 494
OY 491 IANVTOGSMGPFENRSTKVVVAVASGEADVEMACPHLSGRHGGGGRHDEEDVHYE 550


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QY 296 ANPNAPVLPHTLDDADALLVYIGRGALKMIHNDRESYNLECGDVIRIPACTTYLIINRD 355
Db 273 DNQNLRYAKISMPVNTPGQFEDFPASSRDQSSYLQGSRNLTLEAFNAEFNEIRVYLE 332
QY 356 NNERLHTIAKFIQTISTPGQYKEFPAGQNPPEYLTSTFSKEITLEALNTQTEKLRGYE-- 413
Db 333 ENAGGEQEEERGQRRSTRSSDNEGVIYKSKENHVOELTKHAKSVSKGSEEDITNPINL 392
QY 414 ---GQGRE-GVI---IRASQEQ--IRELTRDDS-E-SRH-WHI-RRGES-S-RGPNL 457
Db 393 RDGEPRDISNNPGRLEFVYKPPDKKNPOLDMLCVCETIKGALMLPHNSKAWIYVYNK 452
QY 458 FNKRPLYSNNKIGQAYEVKPED-TRQLODMDLSFIANVTQSGMMGPFFNTRSTKVVVAS 516
Db 453 GTGNLELVAVRKQEQQGRGREQEWEEDEEEDSEEGSNREYARYTARLKEGDFVIMPAAHP 512
QY 517 GEADVEMACPHLSGRHGRGGKRRHEEDVHYE---QVR---ARLSKREAIYVLAGHP 569
Db 513 VA-1NASSE-LHLIGGINAENNRIFLAGDKDNVIDQIEKQAKDLAFPGSGEOVEKLIK 570
QY 570 VVEVSSGNENLLLEAFGINAQNHNENFLAGRERNVLOQIEQAMELAFAPRKEVEESFN 629
Db 571 NQRES-HFVSARPOSQSSPSPEKEDQ 595
QY 630 SODOSTIFFPGPROHOQOSPRSTKQOQ 655

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Search completed: Sat May 13 08:01:29 2000
 Job time : 28 secs.

